

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Degli-Esposti, Mariapia
 Goodwin, Raymond
- 10 (ii) TITLE OF INVENTION: Novel Receptor That Causes Cell Death
- 10 (iii) NUMBER OF SEQUENCES: 6
- 15 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Immunex
 (B) STREET: 51 University Street
 (C) CITY: Seattle
 (D) STATE: WA
 (E) COUNTRY: USA
 (F) ZIP: 98101
- 20 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: Apple Power Macintosh
 (C) OPERATING SYSTEM: Apple Operating System 7.5.3
 (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
- 25 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE: 03 OCTOBER 1997
 (C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: USSN 60/044,456
 (B) FILING DATE: 04 OCTOBER 1996
 (C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Perkins, Patricia Anne
 (B) REGISTRATION NUMBER: 34,693
 (C) REFERENCE/DOCKET NUMBER: 2849-A
- 40 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 2065870430
- 45 (2) INFORMATION FOR SEQ ID NO:1:
- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1847 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant
- 55 (ii) MOLECULE TYPE: cDNA
- 55 (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- 60 (vii) IMMEDIATE SOURCE:
 (B) CLONE: AIR

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 236..1489

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 CTTTTCAGCC ATACCCGGAT GGTCTCTGTCC TCGCTGGCCG TGATCACGCC GTCCTCCTTG 60
 GGGATGAGCA GCGCGGCCGT GACGGCGTCC TGGTGCCCCCT CGATCTTGCT CAGCAGCACC 120
 10 GGGCGGCTGC TCTGCGGCCT GGAGTGGATT TCGGCCGCCA TGTTCGCGCG GCGACTGCTG 180
 CGGCCTCCTC GGCAGGCAGC CCATCAGCTG ACGCCTGGGC GCCCGTCGGA GGGCT ATG
 Met
 1
 15 GAG CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG CTC CTC CTG 286
 Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu Leu
 5 10 15
 20 GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT CGT AGC CCC AGG TGT 334
 Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg Cys
 20 25 30
 25 GAC TGT GCC GGT GAC TTC CAC AAG AAG ATT GGT CTG TTT TGT TGC AGA 382
 Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys Arg
 35 40 45
 30 GGC TGC CCA GCG GGG CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC 430
 Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys
 50 55 60 65
 35 GGC AAC TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC TGG 478
 Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala Trp
 70 75 80
 40 GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG GCC TGT GAT GAG 526
 Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp Glu
 85 90 95
 45 CAG GCC TCC CAG GTG GCG CTG GAG AAC TGT TCA GCA GTG GCC GAC ACC 574
 Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp Thr
 100 105 110
 45 CGC TGT GGC TGT AAG CCA GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA 622
 Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser Gln
 115 120 125
 50 TGT GTC AGC AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 670
 Cys Val Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly
 130 135 140 145
 55 GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA GAT ACT GAC 718
 Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp
 150 155 160
 55 TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA CAT GGC GAT GGC TGC GTG 766
 Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val
 165 170 175
 60 TCC TGC CCC ACG AGC ACC CTG GGG AGC TGT CCA GAG CGC TGT GCC GCT 814
 Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala

	180	185	190	
5	GTC TGT GGC TGG AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly 195 200 205			862
10	CTT GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA TAC CGC Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg 210 215 220 225			910
15	CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA GAT GAA GCT GGG ATG His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly Met 230 235 240			958
20	GAG GCT CTG ACC CCA CCA CCG GCC ACC CAT CTG TCA CCC TTG GAC AGC Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp Ser 245 250 255			1006
25	GCC CAC ACC CTT CTA GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr 260 265 270			1054
30	GTC CAG TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC CAG Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr Gln 275 280 285			1102
35	GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC CAG TTG CCC AGC Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro Ser 290 295 300 305			1150
40	AGA GCT CTT GGC CCC GCT GCG CCC ACA CTC TCG CCA GAG TCC CCA Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser Pro 310 315 320			1198
45	GCC GGC TCG CCA GCC ATG ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp 325 330 335			1246
50	GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr 340 345 350			1294
55	CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC GGC Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile Gly 355 360 365			1342
60	CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG CAG Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln 370 375 380 385			1390
	CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG GGG Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly 390 395 400			1438
	CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro 405 410 415			1486
	TGA CACGGCGCCC ACTTGCCACC TAGGCGCTCT GGTGGCCCTT GCAGAAGGCC			1539
	*			

TAAGTACGGT TACTTATGCG TGTAGACATT TTATGTCACT TATTAAGCCG CTGGCACGGC 1599
CCTGCGTAGC AGCACCAAGCC GGCCCCACCC CTGCTCGCCC CTATCGCTCC AGCCAAGGCG 1659
5 AAGAACGACG AACGAATGTC GAGAGGGGGT GAAGACATTT CTCAACTTCT CGGCCGGAGT 1719
TTGGCTGAGA TCGCGGTATT AAATCTGTGA AAGAAAACAA AAAAAAAA ACCGGAATTG 1779
10 GATATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGC CCGGTACCCA ATTGCCCTA 1839
TAGTGAGT 1847

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
1 5 10 15
Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
20 25 30
30 Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
35 40 45
Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
50 55 60
Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
65 70 75 80
40 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
85 90 95
Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
100 105 110
45 Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
115 120 125
50 Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
130 135 140
Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
145 150 155 160
55 Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
165 170 175
Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala
180 185 190
60 Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala

195 200 205

Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
210 215 220

5 Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
225 230 235 240

Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
10 245 250 255

Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
260 265 270

15 Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
275 280 285

Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
290 295 300

20 Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
305 310 315 320

Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
25 325 330 335

Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
340 345 350

30 Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile
355 360 365

Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln
370 375 380

35 Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
385 390 395 400

Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
40 405 410 415

Pro *

45 (2) INFORMATION FOR SEQ ID NO:3:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

55 (vii) IMMEDIATE SOURCE:
 (B) CLONE: FLAG® peptide

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

20 (vii) IMMEDIATE SOURCE:
 (B) CLONE: IgG1 Fc mutein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20 Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

25 Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

30 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

35 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

40 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

45 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

50 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

55 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

60 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

65 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
 145 150 155 160

70 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

75 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

80 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

85 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

5

(2) INFORMATION FOR SEQ ID NO:5:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

 (iii) HYPOTHETICAL: NO

 (iv) ANTI-SENSE: NO

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Murine AIR

 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 7..1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30	GTG GAC ATG GAG GCA CGG CTG CTG CGG GGC TGC GTG GTG GAG CCT CTG Met Glu Ala Arg Leu Leu Arg Gly Cys Val Val Glu Pro Leu 1 5 10	48
35	TTC CTA CCA CTG CTG CTG CTG CTG CTG CTG CTT GGT GGC CAG GGC Phe Leu Pro Leu Leu Leu Leu Leu Leu Leu Gly Gly Gln Gly 15 20 25 30	96
40	CAG GGC GGC ATG TCT GGC AGG TGT GAC TGT GCC AGT GAG TCC CAG AAG Gln Gly Gly Met Ser Gly Arg Cys Asp Cys Ala Ser Glu Ser Gln Lys 35 40 45	144
45	AGG TAT GGC CCG TTT TGT TGC AGG GGC TGC CCA AAG GGA CAC TAC ATG Arg Tyr Gly Pro Phe Cys Cys Arg Gly Cys Pro Lys Gly His Tyr Met 50 55 60	192
50	AAG GCC CCC TGC GCA GAA CCC TGT GGC AAC TCC ACC TGC CTT CCC TGT Lys Ala Pro Cys Ala Glu Pro Cys Gly Asn Ser Thr Cys Leu Pro Cys 65 70 75	240
55	CCC TCG GAC ACC TTC TTG ACC AGA GAC AAC CAC TTT AAG ACT GAC TGT Pro Ser Asp Thr Phe Leu Thr Arg Asp Asn His Phe Lys Thr Asp Cys 80 85 90	288
60	ACC CGC TGC CAA GTC TGT GAT GAA GAG GCC CTT CAA GTG ACC CTT GAG Thr Arg Cys Gln Val Cys Asp Glu Glu Ala Leu Gln Val Thr Leu Glu 95 100 105 110	336
65	AAC TGC TCG GCA AAG TCG GAC ACC CAC TGT GGC TGC CAG TCA GGC TGG Asn Cys Ser Ala Lys Ser Asp Thr His Cys Gly Cys Gln Ser Gly Trp 115 120 125	384

	TGT GTT GAC TGC TCC ACC GAG CCA TGT GGG AAA AGC TCA CCT TTC TCT Cys Val Asp Cys Ser Thr Glu Pro Cys Gly Lys Ser Ser Pro Phe Ser 130 135 140	432
5	TGT GTC CCA TGC GGG GCT ACA ACA CCA GTC CAT GAG GCT CCA ACC CCC Cys Val Pro Cys Gly Ala Thr Thr Pro Val His Glu Ala Pro Thr Pro 145 150 155	480
10	CGG CCC TGC CTG CCT GGC TTC TAT ATA CGT GGC AAT GAC TGC ACG TCC Arg Pro Cys Leu Pro Gly Phe Tyr Ile Arg Gly Asn Asp Cys Thr Ser 160 165 170	528
15	TGC CCC ACG GGC TTC AGC AGC GTT TGC CCT AAG GCT TGC ACT GCT GTC Cys Pro Thr Gly Phe Ser Ser Val Cys Pro Lys Ala Cys Thr Ala Val 175 180 185 190	576
20	TGT GGC TGG AAG CAG ATG TTT TGG GTC CAG GTG CTT CTA GGA GTC GCG Cys Gly Trp Lys Gln Met Phe Trp Val Gln Val Leu Leu Gly Val Ala 195 200 205	624
25	TTC CTT TTT GGG GCT ATC CTG ATC TGT GCA TAT TGT CGA TGG CAG CCT Phe Leu Phe Gly Ala Ile Leu Ile Cys Ala Tyr Cys Arg Trp Gln Pro 210 215 220	672
30	TGT AAG GCC GTG GTC ACT GCA GAC ACA GCT GGG ACG GAG ACC CTG GCC Cys Lys Ala Val Val Thr Ala Asp Thr Ala Gly Thr Glu Thr Leu Ala 225 230 235	720
35	TCA CCA CAG ACT GCC CAT CTC TCA GCC TCA GAC AGC GCC CAC ACC CTC Ser Pro Gln Thr Ala His Leu Ser Ala Ser Asp Ser Ala His Thr Leu 240 245 250	768
40	CTG GCA CCT CCA AGC AGT ACT GGG AAA ATC TGT ACC ACT GTC CAG TTG Leu Ala Pro Pro Ser Ser Thr Gly Lys Ile Cys Thr Thr Val Gln Leu 255 260 265 270	816
45	GTA GGC AAC AAC TGG ACC CCT GGC TTA TCC CAG ACT CAG GAG GTG GTC Val Gly Asn Asn Trp Thr Pro Gly Leu Ser Gln Thr Gln Glu Val Val 275 280 285	864
50	TGC GGA CAG GCC TCA CAA CCC TGG GAT CAG CTG CCA AAC AGA ACT CTT Cys Gly Gln Ala Ser Gln Pro Trp Asp Gln Leu Pro Asn Arg Thr Leu 290 295 300	912
55	GGA ACT CCT CTG GCA TCT CCG CTC TCG CCA GCG CCC CCT GCG GGC TCT Gly Thr Pro Leu Ala Ser Pro Leu Ser Pro Ala Pro Pro Ala Gly Ser 305 310 315	960
60	CCG GCT GCT GTG CTC CAG CCT GGC CCG CAG CTC TAC GAT GTG ATG GAT Pro Ala Ala Val Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp 320 325 330	1008
	GCG GTC CCA GCA CGA AGG TGG AAG GAG TTC GTG CGC ACG CTG GGG CTG Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu 335 340 345 350	1056
	CGG GAA GCG GAA ATT GAA GCC GTG GAG GTG GAA ATC TGC CGC TTC CGA Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile Cys Arg Phe Arg 355 360 365	1104
	GAC CAG CAG TAT GAG ATG CTC AAG CGC TGG CGT CAG CAG CAG CCT GCA	1152

	Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala			
	370	375	380	
5	GGC CTC GGT GCC ATC TAT GCG GCT CTG GAG CGC ATG GGT CTG GAA GGC		1200	
	Gly Leu Gly Ala Ile Tyr Ala Ala Leu Glu Arg Met Gly Leu Glu Gly			
	385	390	395	
10	TGT GCC GAG GAC CTG CGC AGC CGC CTG CAG CGT GGC CCG TGATGCGGCC		1249	
	Cys Ala Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro			
	400	405	410	
	GC		1251	
15	(2) INFORMATION FOR SEQ ID NO:6:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 411 amino acids			
20	(B) TYPE: amino acid			
	(D) TOPOLOGY: linear			
	(ii) MOLECULE TYPE: protein			
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:			
	Met Glu Ala Arg Leu Leu Arg Gly Cys Val Val Glu Pro Leu Phe Leu			
	1	5	10	15
30	Pro Leu Leu Leu Leu Leu Leu Leu Gly Gly Gln Gly Gln Gly			
	20	25	30	
	Gly Met Ser Gly Arg Cys Asp Cys Ala Ser Glu Ser Gln Lys Arg Tyr			
	35	40	45	
35	Gly Pro Phe Cys Cys Arg Gly Cys Pro Lys Gly His Tyr Met Lys Ala			
	50	55	60	
40	Pro Cys Ala Glu Pro Cys Gly Asn Ser Thr Cys Leu Pro Cys Pro Ser			
	65	70	75	80
	Asp Thr Phe Leu Thr Arg Asp Asn His Phe Lys Thr Asp Cys Thr Arg			
	85	90	95	
45	Cys Gln Val Cys Asp Glu Glu Ala Leu Gln Val Thr Leu Glu Asn Cys			
	100	105	110	
	Ser Ala Lys Ser Asp Thr His Cys Gly Cys Gln Ser Gly Trp Cys Val			
	115	120	125	
50	Asp Cys Ser Thr Glu Pro Cys Gly Lys Ser Ser Pro Phe Ser Cys Val			
	130	135	140	
	Pro Cys Gly Ala Thr Thr Pro Val His Glu Ala Pro Thr Pro Arg Pro			
55	145	150	155	160
	Cys Leu Pro Gly Phe Tyr Ile Arg Gly Asn Asp Cys Thr Ser Cys Pro			
	165	170	175	
60	Thr Gly Phe Ser Ser Val Cys Pro Lys Ala Cys Thr Ala Val Cys Gly			
	180	185	190	

Trp Lys Gln Met Phe Trp Val Gln Val Leu Leu Gly Val Ala Phe Leu
195 200 205

5 Phe Gly Ala Ile Leu Ile Cys Ala Tyr Cys Arg Trp Gln Pro Cys Lys
210 215 220

Ala Val Val Thr Ala Asp Thr Ala Gly Thr Glu Thr Leu Ala Ser Pro
225 230 235 240

10 Gln Thr Ala His Leu Ser Ala Ser Asp Ser Ala His Thr Leu Leu Ala
245 250 255

Pro Pro Ser Ser Thr Gly Lys Ile Cys Thr Thr Val Gln Leu Val Gly
15 260 265 270

Asn Asn Trp Thr Pro Gly Leu Ser Gln Thr Gln Glu Val Val Cys Gly
275 280 285

Gln Ala Ser Gln Pro Trp Asp Gln Leu Pro Asn Arg Thr Leu Gly Thr
20 290 295 300

Pro Leu Ala Ser Pro Leu Ser Pro Ala Pro Pro Ala Gly Ser Pro Ala
305 310 315 320

25 Ala Val Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val
325 330 335

Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu
30 340 345 350

30 Ala Glu Ile Glu Ala Val Glu Val Glu Ile Cys Arg Phe Arg Asp Gln
355 360 365

35 Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu
370 375 380

Gly Ala Ile Tyr Ala Ala Leu Glu Arg Met Gly Leu Glu Gly Cys Ala
385 390 395 400

40 Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
405 410